

C12

General Description References Links Sequence

## General information

Entry name Q9PVY1  
Accession number Q9PVY1 XP-002197933  
Created TrEMBLrel. 13, 1-MAY-2000  
Sequence update TrEMBLrel. 13, 1-MAY-2000  
Annotation update TrEMBLrel. 21, 1-JUN-2002

P.D. 01-05-2000

P. 1-2

2

## Description and origin of the Protein

Description XFGF-20.  
Gene name(s) XFGF-20.  
Organism source *Xenopus laevis* (African clawed frog).  
Taxonomy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; *Xenopus*.  
NCBI TaxID 8355

## References

- [1] Koga,C., Adati,N., Nakata,K., Mikoshiba,K., Furuhashi,Y., Sato,S., Tei,H., Sakaki,Y., Kurokawa,T., Shiokawa,K., Yokoyama,K.K.,  
Characterization of a novel member of the FGF family, XFGF-20, in *Xenopus laevis*.  
(1999) *Biochem. Biophys. Res. Commun.* 261:756-765

Position SEQUENCE FROM N.A.

Medline 99373151

PubMed 10441498

## Database cross-references

EMBL AB012615; BAA83474.1; -.  
HSSP P31371; 1G82.  
InterPro IPR002209; HB/F\_growthfact.  
IPR002348; IL1\_HBGF.  
Pfam PF00167; FGF; 1.  
PRINTS PR00262; IL1HBGF.  
ProDom PD000831; HB/F\_growthfact; 1.  
SMART SM00442; FGF; 1.  
PROSITE PS00247; HBGF\_FGF; 1.

## Sequence information

Length: 208 aa, molecular weight: 23438 Da, CRC64 checksum: 268881D36E757D4D

MAPLADVGT	LGGYDALGQV	GSHFLLP	PAK	DSPLLFNDPL	AQSERLSRSA	PSDLSHLQGI	60
LRRRLQYLCRT	GFHLQILPDG	NVQGT	RQDHS	RFGILEFISV	AIGLV	SIRGV	120
KGELFGSEKL	TSECIFREQF	EENWYNTYSS	NLYKHGDSGR	RYFVALNKDG	TPRDG	TRAKR	180
HQKFTHFLPR	PVDPEKVP	PEL	YKDL	MGYS			208

//

General Description References Links Sequence

>>SWALL:09PVY1 XFGF-20.

initn: 1061 initl: 976 opt: 1169 Z-score: 1387.1 bits: 263.7 E(): 3.4e-69  
Smith-Waterman score: 1169; 80.569% identity (81.731% ungapped) in 211 aa overlap  
(1-211:1-208)

SA3535 MAPLAIEVGGFLGGLGLELQQVGSHFLLPPAGERPPLLGERSSAAERSARGGPGAQLAHL  
::: : :: : : : : : : : . : : . : : : : :  
SWALL: MAPLADVTGLGGYDALGO-VGSHFLLPPAKDSPLLFNPLAQSERLSRSAP--SDLSTH

SA3535 HGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSFGILEFISVAVGLVSIRGVDSGLYL  
SWALL: QGILRRRQLYCRTGFHLQILPDGNVQGTRQDHSRFGILEFISVAIGLVSIRGVDTGLYL

```

          130      140      150      160      170      180
SA3535 MNDKGELYGSEKLTSECFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR
      .....
SWALL: MNDKGELFGSEKLTSECFREQFEENWNTYSSNLYKHGDSGRRYFVALNKDGTPRDGR
      120      130      140      150      160      170

```

```

              190             200             210
SA3535 SKRHQKFTHTFLPRPVDPERVPELYKDLLMYT
      .:::::::::::::::::::::::::: ..
SWALL: AKRHQKFTHTFLPRPVDPEKVPELYKDLMGYS
       180           190           200

```